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|--|----|
| Other sequence(s) detected in Swiss-Prot | 1. |
| Last update | |
| November 1995 / Pattern and text revised. | |
| References | |
| [1] Futai M., Noumi T., Maeda M. Annu. Rev. Biochem. 58:111-136(1989). | |
| [2] Senior A.E. Physiol. Rev. 68:177-231(1988). | |
| [3] Miki J., Maeda M., Mukohata Y., Futai M. FEBS Lett. 232:221-226(1988). | |
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General information about the entry

| | |
|---------------------------------------|---|
| Entry name | ATPG_ECOLI |
| Primary accession number | P00837 |
| Secondary accession number | P00838 |
| Entered in Swiss-Prot in | Release 01, July 1986 |
| Sequence was last modified in | Release 01, July 1986 |
| Annotations were last modified in | Release 42, September 2003 |
| Name and origin of the protein | |
| Protein name | ATP synthase gamma chain |
| Synonym | EC 3.6.3.14 |
| Gene name | ATPG or UNCG or PAPC or <u>B3733</u> or <u>C4659</u> or <u>Z5231</u> or ECS4675 or SF3813 |
| From | <u>Escherichia coli</u> [TaxID: <u>562</u>] <u>Escherichia coli O6</u> [TaxID: <u>217992</u>] <u>Escherichia coli O157:H7</u> [TaxID: <u>83334</u>] <u>Shigella flexneri</u> [TaxID: <u>623</u>] |
| Taxonomy | <u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Enterobacteriales</u> ; <u>Enterobacteriaceae</u> ; <u>Escherichia</u> . |

References

- [1] SEQUENCE FROM NUCLEIC ACID.
SPECIES=E.coli;
MEDLINE=85121806; PubMed=6395859; [NCBI, ExPASy, EBI, Israel, Japan]
Walker J.E., Gay N.J., Saraste M., Eberle A.N.;
"DNA sequence around the Escherichia coli unc operon. Completion of the sequence of a 17 kilobase segment containing asnA, oriC, unc, glmS and phoS."
Biochem. J. 224:799-815(1984).
- [2] SEQUENCE FROM NUCLEIC ACID.
SPECIES=E.coli;
MEDLINE=82059507; PubMed=6272217; [NCBI, ExPASy, EBI, Israel,

| | |
|-----|--|
| | <p><u>Japan]</u> <u>Saraste M., Gay N.J., Eberle A., Runswick M.J., Walker J.E.:</u> "The atp operon: nucleotide sequence of the genes for the gamma, beta, and epsilon subunits of Escherichia coli ATP synthase." <u>Nucleic Acids Res. 9:5287-5296(1981).</u></p> |
| [3] | <p>SEQUENCE FROM NUCLEIC ACID. SPECIES=E.coli; MEDLINE=82134798; PubMed=6277310; [<u>NCBI</u>, <u>ExPASy</u>, <u>EBI</u>, <u>Israel</u>, <u>Japan]</u> <u>Kanazawa H., Kayano T., Mabuchi K., Futai M.:</u> "Nucleotide sequence of the genes coding for alpha, beta and gamma subunits of the proton-translocating ATPase of Escherichia coli." <u>Biochem. Biophys. Res. Commun. 103:604-612(1981).</u></p> |
| [4] | <p>SEQUENCE FROM NUCLEIC ACID. SPECIES=E.coli; STRAIN=K12 / MG1655; MEDLINE=93315143; PubMed=7686882; [<u>NCBI</u>, <u>ExPASy</u>, <u>EBI</u>, <u>Israel</u>, <u>Japan]</u> <u>Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.:</u> "DNA sequence and analysis of 136 kilobases of the Escherichia coli genome: organizational symmetry around the origin of replication." <u>Genomics 16:551-561(1993).</u></p> |
| [5] | <p>SEQUENCE FROM NUCLEIC ACID. SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928; MEDLINE=22388234; PubMed=12471157; [<u>NCBI</u>, <u>ExPASy</u>, <u>EBI</u>, <u>Israel</u>, <u>Japan]</u> <u>Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.:</u> "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli." <u>Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).</u></p> |
| [6] | <p>SEQUENCE FROM NUCLEIC ACID.</p> |

| | |
|-----|---|
| | <p>SPECIES=E.coli;</p> <p>STRAIN=O157:H7 / EDL933 / ATCC 700927;</p> <p>MEDLINE=21074935; PubMed=11206551; [NCBI, ExPASy, EBI, Israel, Japan]</p> <p>Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;</p> <p>"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";</p> <p>Nature 409:529-533(2001).</p> |
| [7] | <p>SEQUENCE FROM NUCLEIC ACID.</p> <p>SPECIES=E.coli;</p> <p>STRAIN=O157:H7 / RIMD 0509952;</p> <p>MEDLINE=21156231; PubMed=11258796; [NCBI, ExPASy, EBI, Israel, Japan]</p> <p>Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;</p> <p>"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";</p> <p>DNA Res. 8:11-22(2001).</p> |
| [8] | <p>SEQUENCE OF <u>261-287</u> FROM NUCLEIC ACID.</p> <p>SPECIES=E.coli;</p> <p>MEDLINE=90202983; PubMed=2138624; [NCBI, ExPASy, EBI, Israel, Japan]</p> <p>Iwamoto A., Miki J., Maeda M., Futai M.;</p> <p>"H(+)-ATPase gamma subunit of Escherichia coli. Role of the conserved carboxyl-terminal region.";</p> <p>J. Biol. Chem. 265:5043-5048(1990).</p> |
| [9] | <p>SEQUENCE FROM NUCLEIC ACID.</p> <p>SPECIES=S.flexneri;</p> <p>STRAIN=301 / Serotype 2a;</p> <p>MEDLINE=22272406; PubMed=12384590; [NCBI, ExPASy, EBI, Israel,</p> |

Japan]

Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Yu J.;

"Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).

[10] X-RAY CRYSTALLOGRAPHY (4.4 ANGSTROMS).

SPECIES=E.coli;

MEDLINE=20040613; PubMed=10570135; [NCBI, ExPASy, EBI, Israel, Japan]

Hausrath A.C., Grueber G., Matthews B.W., Capaldi R.A.;

"Structural features of the gamma subunit of the Escherichia coli F(1) ATPase revealed by a 4.4-A resolution map obtained by X-ray crystallography.";

Proc. Natl. Acad. Sci. U.S.A. 96:13697-13702(1999).

Comments

FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CF(0) COMPLEX.

CATALYTIC ACTIVITY: $\text{ATP} + \text{H}_2\text{O} + \text{H}^+(\text{In}) = \text{ADP} + \text{phosphate} + \text{H}^+(\text{Out})$.

SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.

SIMILARITY: Belongs to the ATPase gamma chain family.

CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS AND VARIOUS OTHER ERRORS.

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Cross-references

| | |
|------|--|
| EMBL | X01631; CAA25781.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | J01594; AAA24736.1; [EMBL / GenBank / DDBJ] ALT_FRAME. [CoDingSequence] |
| | V00267; CAA23526.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | M25464; AAA83874.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | V00312; CAA23597.1; [EMBL / GenBank / DDBJ] ALT_FRAME. [CoDingSequence] |
| | L10328; AAA62085.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | AE000450; AAC76756.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence] |
| | AE016769; AAN83091.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence] |
| | AE005605; AAG58936.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence] |
| | AP002566; BAB38098.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence] |
| | M34095; AAA24742.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | AE015388; AAN45253.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence] |
| PIR | A01038; PWECG. |
| | C91213; C91213. |
| | D86059; D86059. |
| PDB | 1D8S; 03-DEC-99. [ExPASy / RCSB] |
| | 1FS0; 01-MAY-01. [ExPASy / RCSB] |
| | <u>Detailed list of linked structures.</u> |

| | |
|--------------|--|
| EcoGene | EG10104 ; atpG. |
| EcoCyc | EG10104 ; atpG. |
| CMR | P00837 ; B3733. |
| InterPro | IPR000131 ; ATPase_gamma. Graphical view of domain structure. |
| Pfam | PF00231 ; ATP-synt; 1. |
| PRINTS | PR00126 ; ATPASEGAMMA. |
| TIGRFAMs | TIGR01146 ; ATPsyn_F1gamma; 1. |
| PROSITE | PS00153 ; ATPASE_GAMMA; 1. |
| ProDom | [Domain structure / List of seq. sharing at least 1 domain] |
| HOBACGEN | [Family / Alignment / Tree] |
| BLOCKS | P00837 . |
| ProtoNet | P00837 . |
| ProtoMap | P00837 . |
| PRESAGE | P00837 . |
| DIP | P00837 . |
| ModBase | P00837 . |
| SWISS-2DPAGE | Get region on 2D PAGE. |

Keywords

ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; 3D-structure; Complete proteome.

Features

None

Sequence information

| | | |
|-------------------|-------------------------------|---|
| Length: 287 AA | Molecular weight: 31577 Da | CRC64: 2417A4B8FBDB8EF8 [This is a checksum on the sequence] |
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| 10 | 20 | 30 | 40 | 50 | 60 |
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| 70 | 80 | 90 | 100 | 110 | 120 |
| LEYKHPYLED | RDVKRVGYLV | VSTDRGLCGG | LNINLFKKLL | AEMKTWTDKG | VQCDLAMIGS |
| 130 | 140 | 150 | 160 | 170 | 180 |
| KGVSTFFNSVG | GNVVAQVTGM | GDNPSSLSELI | GPVKVMLQAY | DEGRLDKLYI | VSNKFINTMS |
| 190 | 200 | 210 | 220 | 230 | 240 |
| QVPTISQLLP | LPASDDDDLK | HKSWDYLYEP | DPKALLDTLL | RRYVESQVYQ | GVVENLASEQ |
| 250 | 260 | 270 | 280 | | |
| AARMVAMKAA | TDNGGSLIKE | LQLVYNKARQ | ASITQELTEI | VSGAAAV | |

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NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query length: 289 AA

Date run: 2003-06-11 14:57:44 UTC+0100 on sib-blast.unil.ch

Program: NCBI BLASTP 2.2.5 [Nov-16-2002]

Database: XXtremblnew; XXtrembl; XXswissprot

1,135,895 sequences; 361,048,751 total letters

Swiss-Prot Release 41.11 of 06-Jun-2003

TrEMBL Release 23.15 of 06-Jun-2003

TrEMBL_new of 06-Jun-2003

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

| Db AC | Description | Score | E-value |
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| <input type="checkbox"/> sp Q9L6B6 | ATPG_PASMU ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 555 | e-157 |
| <input type="checkbox"/> sp P43716 | ATPG_HAEIN ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 456 | e-127 |
| <input type="checkbox"/> tr Q9KNH4 | ATP synthase F1, gamma subunit [VC2765] [Vibrio cholerae] | 388 | e-107 |
| <input type="checkbox"/> sp P00837 | ATPG_ECOLI ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 385 | e-106 |
| <input type="checkbox"/> tr Q9RFL4 | ATP synthase subunit gamma [ATPG] [Salmonella typhimur... | 385 | e-106 |
| <input type="checkbox"/> tn AAP18944 | Membrane-bound ATP synthase, F1 sector, gamma-subuni... | 385 | e-106 |
| <input type="checkbox"/> tr Q8Z9S5 | ATP synthase gamma subunit protein (EC 3.6.1.34) (Memb... | 384 | e-106 |
| <input type="checkbox"/> tr Q8ZKW8 | Membrane-bound ATP synthase, F1 sector, gamma-subunit ... | 384 | e-106 |

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|--------------------------|-----------------------------|---|---------------------|-------|
| <input type="checkbox"/> | tr Q8E8B9 | ATP synthase F1, gamma subunit [ATPG] [Shewanella onei... | 382 | e-105 |
| <input type="checkbox"/> | tr Q8DDG9 | ATP synthase F1, gamma subunit [VV11020] [Vibrio vulni... | 381 | e-105 |
| <input type="checkbox"/> | tr Q8Z2Q5 | ATP synthase gamma subunit [STY3912] [Salmonella typhi] | 380 | e-104 |
| <input type="checkbox"/> | tn AAO71150 | ATP synthase gamma subunit [atpG] [Salmonella typhi] | 380 | e-104 |
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| <input type="checkbox"/> | tr Q87KA7 | ATP synthase F1, gamma subunit [VP3070] [Vibrio paraha... | 377 | e-104 |
| <input type="checkbox"/> | tr Q8VV78 | F0F1-ATPase subunit gamma [ATPG] [Colwellia maris (Vib... | 362 | 3e-99 |
| <input type="checkbox"/> | tr Q9HT19 | ATP synthase gamma chain [ATPG] [Pseudomonas aeruginosa] | 360 | 1e-98 |
| <input type="checkbox"/> | tr Q88BX3 | ATP synthase F1, gamma subunit [ATPG] [Pseudomonas put... | 348 | 3e-95 |
| <input type="checkbox"/> | tr Q87TT3 | ATP synthase F1, gamma subunit [ATPG] [Pseudomonas syr... | 344 | 6e-94 |
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| <input type="checkbox"/> | tn CAD84116 | ATP synthase gamma subunit (EC 3.6.3.14) [atpG] [Nit... | 343 | 1e-93 |
| <input type="checkbox"/> | tn AAO91434 | ATP synthase, F1 gamma subunit [atpG] [Coxiella burn... | 328 | 5e-89 |
| <input type="checkbox"/> | tr Q8PCZ6 | ATP synthase gamma chain [ATPG] [Xanthomonas campestri... | 325 | 4e-88 |
| <input type="checkbox"/> | tr Q8PGG6 | ATP synthase gamma chain [ATPG] [Xanthomonas axonopodi... | 322 | 3e-87 |
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| <input type="checkbox"/> | sp P41169 | ATPG_THIFE ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 311 | 5e-84 |
| <input type="checkbox"/> | sp O51873 | ATPG_BUCAP ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 308 | 5e-83 |
| <input type="checkbox"/> | tr Q9PE84 | ATP synthase, gamma chain [XF1144] [Xylella fastidiosa] | 307 | 9e-83 |
| <input type="checkbox"/> | tr Q87E89 | ATP synthase gamma chain [ATPG] [Xylella fastidiosa (s... | 306 | 2e-82 |
| <input type="checkbox"/> | tr Q9JW71 | ATP synthase gamma chain (EC 3.6.1.34) [ATPG] [Neisser... | 293 | 1e-78 |
| <input type="checkbox"/> | tr Q9JXQ1 | ATP synthase F1, gamma subunit [NMB1935] [Neisseria me... | 293 | 2e-78 |
| <input type="checkbox"/> | tr Q9RQ80 | Gamma subunit of membrane-bound ATP synthase [ATPG] [B... | 291 | 6e-78 |
| <input type="checkbox"/> | tr Q8D3J4 | AtpG protein [ATPG] [Wigglesworthia brevipalpis] | 270 | 2e-71 |
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| <input type="checkbox"/> | tn AAP19755 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 228 | 9e-59 |
| <input type="checkbox"/> | tn AAP19743 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 228 | 9e-59 |
| <input type="checkbox"/> | tn AAP19759 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 227 | 1e-58 |
| <input type="checkbox"/> | tn AAP19752 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 227 | 1e-58 |
| <input type="checkbox"/> | tn AAP19745 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 227 | 1e-58 |
| <input type="checkbox"/> | tn AAP19744 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 227 | 1e-58 |
| <input type="checkbox"/> | tn AAP19761 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 227 | 1e-58 |
| <input type="checkbox"/> | tn AAP19742 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 226 | 2e-58 |
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| <input type="checkbox"/> | tn AAP19753 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 226 | 2e-58 |
| <input type="checkbox"/> | tn AAP19751 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 226 | 2e-58 |
| <input type="checkbox"/> | tn AAP19749 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 226 | 2e-58 |
| <input type="checkbox"/> | tn AAP19748 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 226 | 2e-58 |
| <input type="checkbox"/> | tn AAP19747 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 226 | 2e-58 |
| <input type="checkbox"/> | tn AAP19746 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 226 | 2e-58 |
| <input type="checkbox"/> | tn AAP19750 | ATP synthase F1 epsilon subunit (Fragment) [atpG] [H... | 224 | 7e-58 |

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| <input type="checkbox"/> | tn | AAP12170 | ATP synthase gamma chain (EC 3.6.3.14) [BC5307] [Bac... | 207 | 2e-52 |
| <input type="checkbox"/> | tn | AAP29192 | ATP synthase F1, gamma subunit [atpG] [Bacillus anth... | 207 | 2e-52 |
| <input type="checkbox"/> | tr | Q8E5U9 | H+-transporting ATP synthase gamma chain [ATPG] [Strep... | 205 | 6e-52 |
| <input type="checkbox"/> | tn | AAO82318 | ATP synthase F1, gamma subunit [atpG] [Enterococcus ... | 205 | 6e-52 |
| <input type="checkbox"/> | tr | Q9RAU1 | H+-ATPase cytoplasmic F1-part gamma-subunit (H+-ATPase... | 204 | 1e-51 |
| <input type="checkbox"/> | sp | Q9CER9 | ATPG_LACLA ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 204 | 1e-51 |
| <input type="checkbox"/> | tr | Q8E073 | ATP synthase F1, gamma subunit [ATPG] [Streptococcus a... | 202 | 3e-51 |
| <input type="checkbox"/> | tr | O05432 | ATP synthase subunit gamma [ATPG] [Moorella thermoacet... | 201 | 7e-51 |
| <input type="checkbox"/> | tr | O50158 | Proton-translocating ATPase, gamma subunit [ATPG] [Str... | 201 | 1e-50 |
| <input type="checkbox"/> | tr | Q8EM82 | H(+)-transporting ATP synthase gamma chain (EC 3.6.1.3... | 197 | 9e-50 |
| <input type="checkbox"/> | tr | Q9A0I8 | Putative proton-translocating ATPase, gamma subunit (E... | 197 | 9e-50 |
| <input type="checkbox"/> | sp | P09222 | ATPG_BACP3 ATP synthase gamma chain precursor (EC 3.6.... | 196 | 2e-49 |
| <input type="checkbox"/> | tr | Q8K827 | Putative proton-translocating ATPase gamma subunit [SP... | 196 | 2e-49 |
| <input type="checkbox"/> | tr | Q97PT5 | ATP synthase F1, gamma subunit (Proton-translocating A... | 196 | 3e-49 |
| <input type="checkbox"/> | tr | Q52412 | TF1-gamma subunit [thermophilic bacterium PS3] | 196 | 4e-49 |
| <input type="checkbox"/> | tr | Q8RKV3 | H+-ATPase cytoplasmic F1-part gamma-subunit [ATPG] [St... | 194 | 1e-48 |
| <input type="checkbox"/> | sp | P12408 | ATPG_ANASP ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 193 | 2e-48 |
| <input type="checkbox"/> | tr | Q8CNJ6 | ATP synthase gamma chain [SE1701] [Staphylococcus epid... | 193 | 2e-48 |
| <input type="checkbox"/> | tr | Q927W3 | AtpG protein [ATPG] [Listeria monocytogenes, Listeria ... | 193 | 2e-48 |
| <input type="checkbox"/> | sp | P17253 | ATPG_SYNY3 ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 192 | 4e-48 |
| <input type="checkbox"/> | tr | Q99SF4 | ATP synthase gamma chain [ATPG] [Staphylococcus aureus... | 192 | 4e-48 |
| <input type="checkbox"/> | sp | P08450 | ATPG_SYNP6 ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 191 | 1e-47 |
| <input type="checkbox"/> | tn | AAO43198 | Chloroplast ATPase gamma subunit precursor [AtpC] [P... | 190 | 2e-47 |
| <input type="checkbox"/> | sp | P43452 | ATPG_ENTHR ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 190 | 2e-47 |
| <input type="checkbox"/> | sp | P41010 | ATPG_BACCA ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 190 | 2e-47 |
| <input type="checkbox"/> | sp | P29710 | ATPG_PROMO ATP synthase gamma chain, sodium ion specif... | 189 | 3e-47 |
| <input type="checkbox"/> | tr | Q8KAW9 | ATP synthase F1, gamma subunit [ATPG] [Chlorobium tepi... | 189 | 3e-47 |
| <input type="checkbox"/> | tr | Q8DLU1 | H+-transporting ATP synthase gamma chain [ATPC] [Synec... | 188 | 6e-47 |
| <input type="checkbox"/> | sp | Q05384 | ATPG_SYNP1 ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 188 | 8e-47 |
| <input type="checkbox"/> | sp | P42007 | ATPG_BACST ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 188 | 8e-47 |
| <input type="checkbox"/> | sp | Q06908 | ATPG_ODOSI ATP synthase gamma chain, chloroplast precu... | 187 | 1e-46 |
| <input type="checkbox"/> | tr | Q9ZJ02 | Proton-translocating ATPase gamma subunit [Streptococc... | 187 | 2e-46 |
| <input type="checkbox"/> | sp | P95788 | ATPG_STRMU ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 186 | 2e-46 |
| <input type="checkbox"/> | tr | Q8KRU9 | Subunit gamma [ATPG] [Ilyobacter tartaricus] | 184 | 8e-46 |
| <input type="checkbox"/> | tr | Q8RGE1 | ATP synthase gamma chain, sodium ion specific (EC 3.6.... | 184 | 1e-45 |
| <input type="checkbox"/> | sp | Q41075 | ATPG_PHATR ATP synthase gamma chain, chloroplast precu... | 183 | 2e-45 |
| <input type="checkbox"/> | sp | Q10597 | ATPG_MYCTU ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 182 | 4e-45 |
| <input type="checkbox"/> | sp | P56082 | ATPG_HELPHY ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 181 | 7e-45 |
| <input type="checkbox"/> | sp | Q9ZK80 | ATPG_HELPIJ ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 179 | 3e-44 |
| <input type="checkbox"/> | sp | P50006 | ATPG_SPIPL ATP synthase gamma chain (EC 3.6.3.14) [ATP... | 179 | 3e-44 |
| <input type="checkbox"/> | tr | Q8A9U6 | ATP synthase gamma chain [BT0719] [Bacteroides thetaio... | 178 | 6e-44 |

Graphical overview of the alignments

Click here

to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(use ScanProsite for more details about PROSITE matches)

new

| Profile hits | | |
|--------------|---------------------------|-------|
| Pfam hits | ATP | |
| Submission | Matches on query sequence | Match |
| ATPG_PASMU | | |
| ATPG_HAEIN | | |
| Q9KNH4 | | |
| ATPG_ECOLI | | |
| Q9RFL4 | | |
| AA018944 | | |
| Q82955 | | |
| Q8ZKN8 | | |
| Q8E889 | | |
| Q8DDG9 | | |
| Q822Q5 | | |
| AA071150 | | |
| ATPG_VIBAL | | |
| Q87KA7 | | |
| Q8VV78 | | |
| Q9HT19 | | |
| Q888X3 | | |
| Q87TT3 | | |
| Q8XU75 | | |
| CA084116 | | |
| AA091434 | | |
| Q8PC26 | | |
| Q8PGG6 | | |
| ATPG_BUCAI | | |
| ATPG_THIFE | | |
| ATPG_BUCAP | | |
| Q9PE84 | | |
| Q87E89 | | |
| Q9JM71 | | |
| Q9JXQ1 | | |
| Q9RQ80 | | |
| Q8D3J4 | | |
| Q9RQ74 | | |
| Q89B40 | | |
| Q9RQ77 | | |
| AA019756 | | |
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| AA019757 | | |
| AA019755 | | |
| AA019743 | | |
| AA019759 | | |
| AA019752 | | |
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| AA019744 | | |
| AA019761 | | |
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| AA019751 | | |
| AA019749 | | |
| AA019748 | | |
| AA019747 | | |
| AA019746 | | |
| AA019750 | | |
| AA019758 | | |
| ATPG_BACME | | |
| ATPG_BACFI | | |
| ATPG_BACHD | | |
| ATPG_BACSU | | |
| AA012170 | | |
| AA029192 | | |
| Q8E5U9 | | |
| AA082318 | | |
| Q9RAU1 | | |
| ATPG_LACLA | | |
| Q8E073 | | |
| Q85432 | | |
| Q50158 | | |

_PCL XL error

Subsystem: KERNEL

Error: IllegalOperatorSequence

Operator: SetClipToPage

Position: 9096

IPB000131: ATPase_gamma

ATP synthase gamma subunit

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Block IPB000131A

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ID    ATPase_gamma; BLOCK
AC    IPB000131A; distance from previous block=(0,62)
DE    ATP synthase gamma subunit
BL    ITM; width=32; seqs=82; 99.5%=1504; strength=1376
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ATPG  PROMO|P29710 ( 3) GKEIKSRISVQSTRQITKAMEIVSSTKFKKF 22
ATPG  RHORU|P07227 ( 4) LKDLRSRITSVKSTQKITSAMKMVAASRLRRA 10
ATPG  RICPR|O50289 ( 4) LKQLRTRIKSVKSTQKITKAMQLVSASKMTKI 12
ATPG  ANASP|P12408 ( 4) LKSIRDRIQSVKNTKKITEAMRLVAAARVRR 14
ATPG  RHOBL|P05436 ( 4) LKDLKNRIGSVKNTRKITKAMQMVAAAKLRR 8
ATPG  RHOCA|P72246 ( 4) LKDLKNRIVSVKNTRKITKAMQMVAAANIRRA 15
ATPG  SPIPL|P50006 ( 3) LKAIRDRIQSVKNTKKITEAMRLVASAKVRR 10
ATPG  SYNPF|Q05384 ( 4) LKAIRDRIKTIKDTRKITEAMRLVAAAKVRR 17
ATPG  SYNPF|P08450 ( 4) LKAIRDRIKSVNTRKITEAMRLVAAAKVRR 13
ATPG  SYNPF|P17253 ( 4) LKAIRDRIQSVKNTKKITEAMRLVAAAKVRR 9
ATP1  ARATH|Q01908 ( 53) LRELDRIDSVKNTQKITEAMKLVAAGVRR 8
ATP2  ARATH|Q01909 ( 63) IRELDRIDSVKNTQKITEAMRLVAAARVRR 12
ATPG  CHLRE|P12113 ( 37) LKEVRDRIASVKNTQKITDAMKLVAAGVRR 12
ATPG  ODOSE|Q06908 ( 59) ANAIRDRIQSVKNTKKITMAMKLVAAGVRR 11
ATPG  PEA|P28552 ( 54) LKDLKNRIDSVKNTQKITEAMKLVAAGVRR 8
ATPG  PHATR|Q41075 ( 58) ANAIRDRIQSVKNTRKITMAMKLVAAPKVRR 43
ATPG  SPIOL|P05435 ( 44) LRELDRIGSVKNTQKITEAMKLVAAGVRR 8
ATPG  TOBAC|P29790 ( 57) LRDLRDRIESVKNTQKITEAMKLVAAGVRR 8

ATPG  BACCA|P41010 ( 7) LRDIKTRINATKKTSQITKAMEMVSTSKLNRA 10
ATPG  BACFI|P22482 ( 4) LRDIQGRITSTKKTKQITKAMQMVSAAKLNRA 12
ATPG  BACP3|P09222 ( 7) LRDIKTRINATKKTSQITKAMEMVLTSLNRA 15

ATPG  BUCAI|P57123 ( 4) TKEIKNKIVSVTNTKKITKAMEMVAASKMRKT 12
ATPG  BUCAP|O51873 ( 4) KKEIKDQIIISVTNTKKITKAMEMVAASKMRKT 17

ATPG  ECOLI|P00837 ( 4) AKEIRSKIASVQNTQKITKAMEMVAASKMRKS 8
ATPG  THIFE|P41169 ( 4) AKEIRGQIKSVKNTRKITRAMEMVAASKMRRA 12
ATPG  VIBAL|P12990 ( 4) AKEIRNKIGSVKSTQKITKAMEMVAASKMRRS 8

ATPG  MYCGE|P47640 ( 4) IQEIKRRMNTVKSTIKITNAMKMVSRAKFIK 26
ATPG  MYCPN|Q50330 ( 4) IQEIKRKMNTVQSTIKITNAMKMVSRAKFVR 22

ATP3  ARATH|Q96250 ( 45) TQVVRNRMKSVKNIQKITKAMKMVAASKLRAV 24
ATP3  IPOBA|P26360 ( 48) TQVVRNRMKSVKNIQKITKAMKMVAASKLRAI 20

ATPG  BOVIN|P05631 ( 28) LKDITRRLKSIKNIQKITKSMKMVAAGKYARA 13
ATPG  HUMAN|P36542 ( 28) LKDITRRLKSIKNIQKITKSMKMVAAGKYARA 13
ATPG  RAT|P35435 ( 3) LKDITRRLKSIKNIQKITKSMKMVAAGKYARA 13

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| ATPG_KLULA | P49377 | (20) | LREIETRLKSIKNIKIEKITKTMKIVASTRLSKA | 24 |
| ATPG_YEAST | P38077 | (36) | LKEVEMRLKSIKNIKIEKITKTMKIVASTRLSKA | 28 |
| | | | | |
| ATPG_ACEWO | P50005 | (4) | VQDIKPRIKSVNSTMQITHAMELVASAKLRKS | 21 |
| ATPG_BACME | P20602 | (4) | LRDIQTRITSTKKTSSQITKAMEMVSAAKLNRA | 11 |
| ATPG_BACST | P42007 | (7) | LRDIKTRINATKKTSSQITKAMEMVSTSKLNRA | 10 |
| ATPG_BACSU | P37810 | (7) | LRDIKSRTSTKKTSSQITKAMQMVSAAKLNRA | 9 |
| ATPG_ENTHR | P43452 | (5) | LNEIKTRIASTKKTSSQITRAMQMVSAASKLTKS | 11 |
| ATPG_HAEIN | P43716 | (4) | AKEIKTKIASVQSTQKITKAMEMVATSKMRKT | 8 |
| ATPG_HELPY | P56082 | (4) | LRDIRKKIGSVKNTQKITHAMKLVSTSKLRKA | 10 |
| ATPG_HELPJ | Q9ZK80 | (4) | LRDIRKKIGSVKNTQRITHAMKLVSTSKLRKA | 14 |
| ATPG_MYCLE | P45824 | (5) | LRELGRIRSVGSIKKITKAQELIATSRIARA | 18 |
| ATPG_MYCTU | Q10597 | (5) | LRELGRIRSVGSIKKITKAQELIATSRIARA | 27 |
| ATPG_PASMU | Q9L6B6 | (4) | AKEIRTKIASVKSTQKITKAMEMVAASKMRKT | 8 |
| ATPG_STRLI | P50007 | (4) | LRVYKRRIRSVTATKKITKAMEMIAASRVVKA | 17 |
| ATPG_STRMU | P95788 | (5) | LSEIKVRITSTQKTGKITSAMKMWSSAKLVKS | 20 |
| ATPG_DROME | O01666 | (29) | LKMISIRLKSVMNIQKITQSMKMWSAKYARA | 32 |
| O74754 | | (34) | LKEIEQRLKSIKNIKIEKITKTIKTVAQTKLTRA | 38 |
| Q9NE84 | | (5) | LRLYKEKLEGYNRFYSIVKTIKMTMAKFRQA | 100 |
| O21267 | | (4) | TKDFKNRIKSITSIRKITKAMKMWAAASKLRQA | 20 |
| Q9G8R3 | | (4) | PKKLLKQLKSYERFKLLTKAIQMVALSQLSGL | 93 |
| O50141 | | (4) | MKDVKRRIKSVESTMQITKAMQLVASSKMRKA | 14 |
| O50158 | | (5) | LSEIKGKIISTQKTSHITGAMQMVSAAKLTKS | 20 |
| O67829 | | (6) | PRDIKRKIQGIKNTKRITNAMKVVSAAKLRKA | 27 |
| O05432 | | (4) | MRDLKRRIRSVQSTQHITRAMKMWAAAKLRKA | 13 |
| Q52412 | | (3) | LRDIKTRINATKKTSSQITKAMEMVLTSKLNRA | 15 |
| Q9ZJ02 | | (5) | LNDIKNKIASTKNTSQITNAMQMVSAAKLGKS | 15 |
| Q9Z688 | | (6) | LI I I K R R I K S I T N T K K I T N A M G L I A T S N L R K S | 35 |
| Q9X1U6 | | (1) | MLQIKRKINATQSLMKITRAMEMVARAKVRKI | 33 |
| Q9RQ80 | | (4) | IKIEIKTQITSVNTKKITKAMEMVAISKMRKT | 18 |
| Q9RQ77 | | (4) | KKEIKNKINCISNTKKITKAMEMVSIAMKKS | 22 |
| Q9RQ74 | | (4) | IKIEVRNKIKCITNTQKITKAMEMVSIKMKKA | 17 |
| Q9RGY2 | | (5) | LLELKRKIASVKQTGKITEAMRMVSASKLNQT | 22 |
| Q9RFL4 | | (4) | AKEIRSKIASVQNTQKITKAMEMVAASKMRKS | 8 |
| Q9RAU1 | | (5) | LNEIKTKIASTKKTSSQITGAMQMVSAAKLQKA | 13 |
| Q9PR14 | | (3) | LDAMKRKINSVQTTAKITNAMKLVATAKLKRQ | 38 |
| Q9PJ20 | | (4) | LKEIKRKIKSVHNTQKTTNAMKLVSTAKLKKA | 25 |
| Q9PE84 | | (4) | GREIKSKIKSQVNTKRVTRALEMVSASKIRKA | 34 |
| Q9KNH4 | | (4) | AKEIRTKIGSVKSTQKITKAMEMVAASKMRRS | 8 |
| Q9K6H4 | | (4) | LRDIKQRINSTKKTQKITKAMEMVSAAKLNRS | 10 |
| Q9K4D4 | | (5) | LRVYKRRIRSVTATKKITKAMEMIAASRVVKA | 17 |
| Q9JXQ1 | | (4) | GKEILTKIRSVQNTQKITKAMQMVSTSKMRKT | 12 |
| Q9JW71 | | (4) | GKEILTKIRSVQNTQKITKAMQMVSTSKMRKT | 12 |
| Q9HT19 | | (4) | AKEIRSKIASIKSTQKITNAMEKVAVSKMRKA | 18 |
| Q9FDR6 | | (4) | IRELRDRIRSVNSTKKITKAQELIATSRIITKA | 16 |
| Q9FAA4 | | (4) | IRELRDRIRSVNSTKKITKAQELIATSRIITKA | 16 |
| Q9CER9 | | (5) | LNEIKTKIASTKKTSSQITGAMQMVSAAKLQKA | 13 |
| Q9ERA8 | | (28) | LKDITRRLKSIKNIQKITKSMKMWAAAKYARA | 13 |
| Q9D9D7 | | (28) | LKDITRRLKSIKNIQKITKSMKMWAAAKYARA | 13 |
| // | | | | |

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Block IPB000131B

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ID  ATPase_gamma; BLOCK
AC  IPB000131B; distance from previous block=(25,64)
DE  ATP synthase gamma subunit
BL  DGL; width=25; seqs=82; 99.5%=1302; strength=1268
ATPG_BACFI|P22482 ( 73) VKKTGYIVVTSKGLAGGYNSSLR 9
ATPG_MYCGA|P33257 ( 74) STKRLWIVINTQLGLCGSYNTNVGK 49

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| | | | | |
|-------------------|---------------|--------|----------------------------|----|
| <u>ATPG PROMO</u> | <u>P29710</u> | (73) | VKRIGIIVMTSDRGLCGGFNSSTLK | 12 |
| <u>ATPG RHOBL</u> | <u>P05436</u> | (74) | DQIHLLVMTSERGLCGGFNSTIVR | 23 |
| <u>ATPG RHOCA</u> | <u>P72246</u> | (76) | DKVHLLVIMTGERGLCGGFNANIAK | 20 |
| <u>ATPG RHORU</u> | <u>P07227</u> | (76) | DNVHLIVALTANRGLCGGFNGSIIR | 24 |
| <u>ATPG RICPR</u> | <u>O50289</u> | (77) | SKINLLIVMTSERGLCGMFNYSIIK | 32 |
| <u>ATPG SPIPL</u> | <u>P50006</u> | (74) | VKKVGLVVLAGNRGLCGAYNSNIIK | 19 |
| <u>ATPG THIFE</u> | <u>P41169</u> | (73) | VKKAGFLVVTDDRGLCGGLNVNVL | 12 |
| <u>ATPG ANASP</u> | <u>P12408</u> | (75) | VKSVGLLVISGDRGLCGGYNTNVIR | 11 |
| <u>ATPG SYNPI</u> | <u>Q05384</u> | (75) | VKTVALLVVTGDRGLCGGYNTNVIR | 11 |
| <u>ATPG SYNPI</u> | <u>P08450</u> | (75) | VKTVALLVVSGDRGLCGGYNSNVIR | 11 |
| <u>ATPG SYNPI</u> | <u>P17253</u> | (75) | PKAVALLVVTGDRGLCGGYNVNAIK | 26 |
| <u>ATPG BACCA</u> | <u>P41010</u> | (73) | VKKTGYLVITSRGLAGAYNSNVVR | 9 |
| <u>ATPG BACPI</u> | <u>P09222</u> | (74) | VKKTGYLVITSRGLAGAYNSNVLR | 9 |
| <u>ATPG BUCAI</u> | <u>P57123</u> | (73) | TNRIGMIIISTDRGLCGGLNTNLFK | 16 |
| <u>ATPG BUCAP</u> | <u>O51873</u> | (73) | DKRIGIIIVSTDRLCGSLNTNLFK | 12 |
| <u>ATPG ECOLI</u> | <u>P00837</u> | (73) | VKRVGYLVVSTDRLCGGLNINLFK | 10 |
| <u>ATPG VIBAL</u> | <u>P12990</u> | (73) | AKRVGYIIVSTDRLCGGLNINLVK | 11 |
| <u>ATPG MYCGE</u> | <u>P47640</u> | (69) | NQKTLWIMSSSLGCGQHNSNMNK | 39 |
| <u>ATPG MYCPN</u> | <u>Q50330</u> | (69) | NPKTLWVMMSSSLGCGQHNTNMNK | 39 |
| <u>ATP1 ARATH</u> | <u>Q01908</u> | (124) | VKKVALVVVTGDRGLCGGFNNFIIK | 11 |
| <u>ATP2 ARATH</u> | <u>Q01909</u> | (134) | VKRVALVVVTGDKGLCGGFNNAVTK | 18 |
| <u>ATPG CHLRE</u> | <u>P12113</u> | (108) | VKSVLLVLTGDRGLCGGYNNFIIK | 14 |
| <u>ATPG PEA</u> | <u>P28552</u> | (125) | VKKVALVVTGDRGLCGGFNNAILK | 17 |
| <u>ATPG SPIOL</u> | <u>P05435</u> | (115) | VKKVALMVVTGDRGLCGGFNNMLLK | 30 |
| <u>ATPG TOBAC</u> | <u>P29790</u> | (128) | VKKVALVVVTGDRGLCGGFNNYLIK | 15 |
| <u>ATPG ODOSI</u> | <u>Q06908</u> | (130) | VSKVTLVVITGDRGLCGGYNSFMIK | 17 |
| <u>ATPG PHATR</u> | <u>Q41075</u> | (130) | VKKVTLVVITGDRGLCGGYNSFMIK | 15 |
| <u>ATP3 ARATH</u> | <u>Q96250</u> | (102) | VKKSVMVTLSSDKGLCGGINSTVVK | 20 |
| <u>ATP3 IPOBA</u> | <u>P26360</u> | (105) | VKKNVIIITISSDKGLCGGINSTSVK | 21 |
| <u>ATPG BOVIN</u> | <u>P05631</u> | (88) | KKKHLLIIGVSSDRGLCGAIHSSVAK | 14 |
| <u>ATPG HUMAN</u> | <u>P36542</u> | (88) | KKKHLLIIGVSSDRGLCGAIHSSIAK | 14 |
| <u>ATPG RAT</u> | <u>P35435</u> | (63) | KKKHLLIIGVSSDRGLCGAIHSSVAK | 14 |
| <u>ATPG KLULA</u> | <u>P49377</u> | (81) | EKKDLIIAITSDKGLCGSIHSQLAK | 20 |
| <u>ATPG YEAST</u> | <u>P38077</u> | (102) | APKELIVAITSDKGLCGSIHSQLAK | 25 |
| <u>ATPG ACEWO</u> | <u>P50005</u> | (73) | VKKTAYIIITGDKGLAGGYNVNVAK | 11 |
| <u>ATPG BACME</u> | <u>P20602</u> | (73) | VKKTGYIVITSRGLAGAYNSNIIK | 9 |
| <u>ATPG BACST</u> | <u>P42007</u> | (73) | VKKTGYLVITSRGLAGAYNSNVVR | 9 |
| <u>ATPG BACSU</u> | <u>P37810</u> | (76) | VKKTAYLVITSRGLAGAFNSSVLR | 9 |
| <u>ATPG ENTHR</u> | <u>P43452</u> | (85) | VKKTGYIVITADGGLVGGYNSIILK | 22 |
| <u>ATPG HAEIN</u> | <u>P43716</u> | (73) | VKKIGILVISTDRGMCGGLNVNLFK | 15 |
| <u>ATPG HELPY</u> | <u>P56082</u> | (81) | IKKVDIIFITADKGLCGGFNTNTIK | 16 |
| <u>ATPG HELPJ</u> | <u>Q9ZK80</u> | (81) | IKKVDIIFITADKGLCGGFNTNTIK | 16 |
| <u>ATPG MYCLE</u> | <u>P45824</u> | (74) | PKRAGVLVVSSDRGLCGAYNANVFR | 11 |
| <u>ATPG MYCTU</u> | <u>Q10597</u> | (74) | PKRAGVLVVSSDRGLCGAYNANIFR | 11 |
| <u>ATPG PASMU</u> | <u>Q9L6B6</u> | (73) | VKKVGMIVSTDRLCGGLNVNLFK | 12 |
| <u>ATPG STRLI</u> | <u>P50007</u> | (71) | PSRAAVLLLTSDRGLAGAFNSNSIK | 17 |
| <u>ATPG STRMU</u> | <u>P95788</u> | (76) | IKKTAYIVITSDKGLVGAYNSTILK | 12 |

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ATPG DROME|O01666 ( 90) EPKLLIAVTS DRGLCGAVHTGVAR 33
O74754 ( 93) EGKTLMVACSSDKGLCGGIHSSISR 35
Q9NE84 ( 66) QAKAIYIPVMTNRGSCGALNSNVVK 57
O21267 ( 66) VNNKIVVPISSDRGLCGGINTNVVK 22
Q9G8R3 ( 62) DLNYLVLSITVDKSCGPHNGNVLK 100
O50141 ( 72) KNSVLLIIVIAGDRGLAGGFNTNVLK 19
O50158 ( 76) VKKTGYIVITSDKGLVGGYNSKILK 13
O67829 ( 75) ERNVDVILVTADRGLAGAFNSNVIR 19
O05432 ( 73) VKKAGYVLITADRGLAGGYNANLIR 12
Q52412 ( 70) VKKTGYLVITSDRGLAGAYNSNVLR 9
Q9ZJ02 ( 77) VKKSAYIVITSDRGLVGGYNATILK 14
Q9Z688 ( 74) SDKKLYIALTSDSGLCGGFNGAVVT 50
Q9X1U6 ( 66) GNRDLIVVITSDMGLCGSFNSEILR 25
Q9RQ80 ( 73) IKRIGLIIVSSDRGLCGSLNSNLFR 11
Q9RQ77 ( 73) TTKIGIIVISTDRGLCGSLNISLFLK 13
Q9RQ74 ( 73) VKKIGIIIIISTDRGLCGNLNVTFLK 20
Q9RGY2 ( 102) IKTTGFLVVTGDRGLVGSYNSSVIK 15
Q9RFL4 ( 73) VKRVGYLVVSTDRLCGGLNINLFLK 10
Q9RAU1 ( 75) VKKTGYLVITSDRGLVGSYNSNILK 11
Q9PR14 ( 71) KDRTLYITINSTMGLAGSYNYNVNK 40
Q9PJ20 ( 81) IKTVDLIFITADKGLCGGFNIKTLK 21
Q9PE84 ( 74) VKRIGYIVISSDRGLAGGLNNNLFR 10
Q9KNH4 ( 73) AKRVGYIIIISTDRGLCGGLNINLFLK 12
Q9K6H4 ( 73) VKKTGYIVITSDRGLAGAYNSNLIR 9
Q9K4D4 ( 74) PSRAAVLLLTSDRGLAGAFNSNSIK 17
Q9JXQ1 ( 74) IRRVGFILITSDKGLCGGLNANVLK 14
Q9JW71 ( 74) IRRVGFILITSDKGLCGGLNANVLK 14
Q9HT19 ( 73) VKRVGYIVVSSDRGLCGGLNINLFLK 9
Q9FDR6 ( 73) GKRAAVLVVTS DRGMAGGYNHNVLK 19
Q9FAA4 ( 73) GKRAAVLVVTS DRGMAGGYNHNVLK 19
Q9CER9 ( 75) VKKTGYLVITSDRGLVGGYNSNILK 10
Q9ERA8 ( 88) KKKHLIIGVSSDRGLCGAIHSSVAK 14
Q9D9D7 ( 88) KKKHLIIGVSSDRGLCGAIHSSVAK 14
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Block IPB000131C

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ID  ATPase_gamma; BLOCK
AC  IPB000131C; distance from previous block=(13,21)
DE  ATP synthase gamma subunit
BL  GKR; width=11; seqs=82; 99.5%=790; strength=997
ATPG BACFI|P22482 ( 113) YGIIIMGRIGR 100

ATPG ECOLI|P00837 ( 118) IGSKGVSFENS 11

ATPG MYCGA|P33257 ( 113) VGIKLNSFLRT 49

ATPG THIFE|P41169 ( 118) VGNKGLGFLRR 24

ATPG VIBAL|P12990 ( 118) VGSKATAFFKH 28

ATP3 ARATH|Q96250 ( 147) VGEKAKAIMFR 32

ATP3 IPOBA|P26360 ( 150) LGEKAKAQLVR 20

ATPG ANASP|P12408 ( 120) VGRKAEQYFRR 18
ATPG SPIPL|P50006 ( 119) VGRKAIQHFR 15
ATPG SYNPI|Q05384 ( 120) VGRKAAQYFQR 11
ATPG SYNPI|P08450 ( 120) VGRKAGQYFQR 19
ATPG SYNPI|P17253 ( 120) VGSKAKQYFGR 14

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| | | | | |
|------------|--------|--------|-----------------------|----|
| ATP1 ARATH | Q01908 | (169) | VGKKGNSYFLR | 10 |
| ATP2 ARATH | Q01909 | (179) | VGKKGNAYFSR | 10 |
| ATPG CHLRE | P12113 | (153) | VGRKGAQYFAR | 18 |
| ATPG ODOSI | Q06908 | (175) | IGKKGITYFQR | 12 |
| ATPG PEA | P28552 | (170) | VGRKGNSYFNR | 9 |
| ATPG PHATR | Q41075 | (175) | VGKKGIAYFER | 13 |
| ATPG SPIOL | P05435 | (160) | IGKKGNTYFIR | 16 |
| ATPG TOBAC | P29790 | (173) | VGKKGNSYFIR | 12 |
| | | | | |
| ATPG BACCA | P41010 | (119) | IGRVGLSFFRK | 11 |
| ATPG BACP3 | P09222 | (119) | IGRVGLSFFRK | 11 |
| | | | | |
| ATPG BUCAI | P57123 | (118) | FGLKSLSVFKL | 26 |
| ATPG BUCAP | O51873 | (118) | FGLKSLSVFKL | 26 |
| | | | | |
| ATPG MYCGE | P47640 | (108) | LGRKNQSFWNK | 34 |
| ATPG MYCPN | Q50330 | (108) | LGRKNQSFWNK | 34 |
| | | | | |
| ATPG PROMO | P29710 | (116) | IGKKGRDYCKK | 15 |
| ATPG RHOBL | P05436 | (119) | VGKKGREQLKR | 11 |
| ATPG RHOC | P72246 | (121) | VGKKGRDALRR | 11 |
| ATPG RHORU | P07227 | (121) | IGKKGRDGLKR | 21 |
| ATPG RICPR | O50289 | (122) | IGKKGYEALKR | 21 |
| | | | | |
| ATPG BOVIN | P05631 | (133) | VGDKIRSILHR | 24 |
| ATPG HUMAN | P36542 | (133) | IGDKIRGILYR | 18 |
| ATPG RAT | P35435 | (108) | IGEKIKSILYR | 16 |
| | | | | |
| ATPG KLULA | P49377 | (122) | IGDKVKGQLLR | 26 |
| ATPG YEAST | P38077 | (143) | IGDKIKMQLLR | 21 |
| | | | | |
| ATPG ACEWO | P50005 | (114) | VGSRGRDHFRN | 23 |
| ATPG BACME | P20602 | (118) | IGRVGRDFFVK | 15 |
| ATPG BACST | P42007 | (119) | IGRVGLSFFRK | 11 |
| ATPG BACSU | P37810 | (121) | IGRVGRDFFKK | 11 |
| ATPG ENTHR | P43452 | (130) | IGGTGADFFKA | 17 |
| ATPG HAEIN | P43716 | (118) | IGSKGISFFRS | 9 |
| ATPG HELPY | P56082 | (126) | IGKKGNEYFSF | 12 |
| ATPG HELPJ | Q9ZK80 | (126) | IGKKGNEYFSF | 12 |
| ATPG MYCLE | P45824 | (119) | VGRKALNYYTF | 18 |
| ATPG MYCTU | Q10597 | (119) | VGRKAQNYYSF | 19 |
| ATPG PASMU | Q9L6B6 | (118) | IGSKSINFFQS | 17 |
| ATPG STRLI | P50007 | (116) | VGRRGLAHYNF | 21 |
| ATPG STRMU | P95788 | (121) | IGGMGSDFFRA | 41 |
| ATPG DROME | O01666 | (132) | VGDKSRILSR | 18 |
| O74754 | | (137) | LGEKVRTQLLR | 29 |
| Q9NE84 | | (105) | LGKRGIESLSK | 32 |
| O21267 | | (111) | VGIKAKDQLQR | 16 |
| Q9G8R3 | | (107) | IGRKAKFFFKK | 21 |
| O50141 | | (117) | IGKKAVEYFEK | 15 |
| O50158 | | (120) | IGGIGADFFKA | 24 |
| O67829 | | (120) | VGRKGFQYFTK | 20 |
| O05432 | | (115) | VGRKGRDFFRR | 8 |
| Q52412 | | (115) | IGRVGLSFFRK | 11 |
| Q9ZJ02 | | (122) | IGSVGADFFRA | 13 |
| Q9Z688 | | (116) | VGQKGISYFKR | 15 |
| Q9X1U6 | | (107) | VGLKAINHFKD | 30 |
| Q9RQ80 | | (118) | FGLKS L P V F K L | 38 |
| Q9RQ77 | | (118) | L G S K G V S Y F K S | 12 |
| Q9RQ74 | | (118) | L G L K G L S F F K S | 13 |
| Q9RGY2 | | (147) | V G S V G A Q F F K K | 12 |
| Q9RFL4 | | (118) | I G S K G V S F F D S | 19 |
| Q9RAU1 | | (120) | L G G T G A D F F K A | 19 |
| Q9PR14 | | (110) | I G K K G H D F M R L | 30 |
| Q9PJ20 | | (126) | I G K T G I E Y F N F | 16 |

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Q9PE84      ( 119) IGQKASVFFRR  31
Q9KNH4      ( 118) IGSKATAFFNN  21
Q9K6H4      ( 118) IGRTGRDLLKK  27
Q9K4D4      ( 119) VGRRLAHYNF  21
Q9JXQ1      ( 119) FGSKGLMACQS  29
Q9JW71      ( 119) LGSKGLMACQS  25
Q9HT19      ( 118) IGSKGASFFRS   9
Q9FDR6      ( 118) TGKKGVDYYKF  25
Q9FAA4      ( 118) TGKKGVDYYKF  25
Q9CER9      ( 120) LGGTGADFFKA  19
Q9ERA8      ( 133) VGEKIKGILYR  18
Q9D9D7      ( 133) VGEKIKGILYR  18
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Block IPB000131D

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ID  ATPase_gamma; BLOCK
AC  IPB000131D; distance from previous block=(33,72)
DE  ATP synthase gamma subunit
BL  DFP; width=26; seqs=82; 99.5%=1450; strength=1161
ATPG BACFI|P22482 ( 166) DELYVWYNHFVSPITQDVTEMKLLLL  40

ATPG ECOLI|P00837 ( 166) DKLYIVSNKFINTMSQVPTISQLLPL  13
ATPG MYCGA|P33257 ( 196) DTLDRINDKFKPNISFEPGVDVIIPA 100
ATPG MYCGE|P47640 ( 158) DRICMVYTKFKNSLIQQSQLFQVFPF  33
ATPG MYCPN|Q50330 ( 158) DRICIIYTQFKNPLIQHANSFQVFPF  37
ATPG PROMO|P29710 ( 164) DEVYLIYNEFISALSTELIVKKLLPI  32
ATPG RHORU|P07227 ( 171) DVCTLVYNRFQSAISQVVTRQQIIPF  27
ATPG RICPR|O50289 ( 170) SNCIIYFNKFKNAMTQIPTKQKILPI  49
ATPG THIFE|P41169 ( 166) DVVYLVSSRFVNTMLQRATVEQLLPV  27
ATPG VIBAL|P12990 ( 166) DRLYVVFNKFVNTMVQQPTIDQLLPL  13
ATPG CHLRE|P12113 ( 201) DKVELVFTKFI SLINSNPTIQTLLPM  18

ATPG ANASP|P12408 ( 168) DRIELVYTRFVSLVSSRPVIQTLLPL  13
ATPG SPIPL|P50006 ( 167) DRVELIYTKFVSLISSRPVTQTLLPL  13
ATPG SYNP1|Q05384 ( 168) DRVELIYTKFVSLISSKPVVQTLLPL  10
ATPG SYNP6|P08450 ( 168) DRVELVYTKFSLVASNPVVQTLLPL  16
ATPG SYNY3|P17253 ( 168) DRVELIYTRFVSLISSQPVVQTLFPL  12
ATP1 ARATH|Q01908 ( 217) DKVELLYTKFVSLVKSEPVIHTLLPL  13
ATP2 ARATH|Q01909 ( 228) DKVELVYTKFVSLVKS DPVIHTLLPL  13
ATPG PEA|P28552 ( 218) DKVELLYTKFVSLVKS NPIIHTLLPL  15
ATPG SPIOL|P05435 ( 208) DKVEMLYTKFVSLVKS DPVIHTLLPL  16
ATPG TOBAC|P29790 ( 221) DKVELLYTKFVSLVKS EPVIHTLLPL  13

ATPG BACCA|P41010 ( 167) DELYMYYNHYVSAIQQEVTERKLLPL  17
ATPG BACP3|P09222 ( 167) DELYMYYNHYVSAIQQEVTERKLLPL  17

ATPG BUCAI|P57123 ( 166) DKIFIAYNKFHNKMSQYPTITQLLPF  23
ATPG BUCAP|O51873 ( 166) DRLFIAYNKFHNKLSQYPKISQLLPL  17

ATPG RHOBL|P05436 ( 169) DVVTIFYNRFQSVISQVPTAQQVIPA  24

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|------------|----------|--------|-----------------------------|----|
| ATPG RHOC | A P72246 | (171) | DVATIFFSVFQSVISQVPTAKQVIPA | 49 |
| ATPG ODO | S Q06908 | (222) | DAVELLYTKFISLIASSPSARTLIPF | 18 |
| ATPG PHAT | R Q41075 | (222) | DAVELLYTKFVSLIASSPSIRTLVPF | 21 |
| ATPG3 AR | A Q96250 | (194) | DALRIVYNKFHSSVVAFLPTVSTVLSP | 30 |
| ATPG3 IPO | B P26360 | (197) | DALRIVFNKFQSVVSFVPTMSTVLSP | 25 |
| ATPG BOV | I P05631 | (181) | DEGSIIFNFRSVISYKTEEKPIFSL | 22 |
| ATPG HUMAN | P36542 | (181) | DEGSIIFNKFRSVISYKTEEKPIFSL | 22 |
| ATPG RAT | P35435 | (156) | DEGSIIFNQFKSVISYKTEEKPIFSF | 21 |
| ATPG KLUL | A P49377 | (179) | DPISSLSFEPSPNKPVFNAAAIEQSPS | 78 |
| ATPG YEAS | T P38077 | (201) | DPVSSLSFEPSEKPIFNAKTIEQSPS | 90 |
| ATPG ACEW | O P50005 | (162) | DEVYIAYTKFVSTITQHAQMMKLLPL | 17 |
| ATPG BACME | P20602 | (166) | DELYLYYNHFINTISQEVTEKKLLPL | 11 |
| ATPG BACST | P42007 | (167) | DELYMYYNHYVSAIQQEVTERKLLPL | 17 |
| ATPG BACSU | P37810 | (169) | DELHLVYNHFVSAITQEVTEKKLLPL | 10 |
| ATPG ENTHR | P43452 | (178) | DELYVCYNHHINSLTSQFRVEKMLPI | 20 |
| ATPG HAEIN | P43716 | (166) | DAVYIAYNKFNVTMSQKPVVQQLVPL | 16 |
| ATPG HELPY | P56082 | (174) | DKVIIHNGFKNMITQEIRVKTILPI | 23 |
| ATPG HELPJ | Q9ZK80 | (174) | DKVIIHNGFKNMITQEIRVKTILPI | 23 |
| ATPG MYCLE | P45824 | (173) | DELHIVFTEFKSMLSQSTKARRMAPM | 23 |
| ATPG MYCTU | Q10597 | (180) | DELHIVYTEFKSMLSQSAEAHRIAPM | 20 |
| ATPG PASMU | Q9L6B6 | (166) | DVVYLVYNKFINTMSQKPVLEKLIPL | 15 |
| ATPG STRLI | P50007 | (168) | DELHIVYTEFVSMMTQTAVDSRLLPL | 18 |
| ATPG STRMU | P95788 | (169) | DELYVCYSHHINSLTSQVRVEKMLPI | 19 |
| ATPG DROME | O01666 | (180) | TEGKIVYNRFKSVVSYQCSTLPIFSG | 58 |
| O74754 | | (185) | DRIVLVYNKFASAVSFETVMKNLYTT | 69 |
| Q9NE84 | | (153) | DRVHVI FHRCVSAGSQKQCYYNIPSY | 91 |
| Q21267 | | (157) | DTCYLVYNQFRSVLTQNVIESKIASR | 36 |
| Q9G8R3 | | (153) | DRFYII FNRFYSAFTQKVSYYDVCSF | 59 |
| O50141 | | (165) | DAVELVYTTFFVSVMTQEPQHLRILPV | 34 |
| O50158 | | (168) | DELYVCYNHHVNSLTSQVRVQQMLPI | 16 |
| O67829 | | (169) | DRVYLINNEMVTRASYKPQVRVFLPF | 84 |
| O05432 | | (163) | DEVNLTINRFYSPIRQVPMVERLLPI | 37 |
| Q52412 | | (163) | DELYMYYNHYVSAIQQEVTERKLLPL | 17 |
| Q9ZJ02 | | (170) | DELYVCYNHHVNSLTSQMRVEQMLPI | 24 |
| Q9Z688 | | (164) | GEVHVIYTQFLSTVNQKVEVKVLPPI | 35 |
| Q9X1U6 | | (152) | ARVRVIFSRFKNVLIQRPEVHELLPI | 35 |
| Q9RQ80 | | (166) | DKIFIAYNEFHKNMSQYPKIIQLLPL | 19 |
| Q9RQ77 | | (166) | DKLFLSYNQFKNTLVYIPVIMQLLPL | 27 |
| Q9RQ74 | | (166) | DRLFLAYNKFKSTLIQIPSIQLLPL | 16 |
| Q9RGY2 | | (195) | DQLYVCYTHHVNSLSSAFRVEKMLPI | 28 |
| Q9RFL4 | | (166) | DKLYIVSNKFINTMSQVPTISQLLPL | 13 |
| Q9RAU1 | | (168) | DELYVCYNHHVNSLVSEARMEKMLPI | 18 |
| Q9PR14 | | (160) | NKICIIYTKFINAITFEVSVIDVLPF | 36 |
| Q9PJ20 | | (174) | DEVILVHNGYKNMITQELKINHILIPV | 41 |
| Q9PE84 | | (167) | DRVYLVYNRFINTMVQKASFDQLLPL | 19 |
| Q9KNH4 | | (166) | DRLYLVFNQFVNTMVQKPKIDQLLPL | 14 |
| Q9K6H4 | | (166) | DELYIWNHNFVSPKQDVTEKKVLPPL | 18 |
| Q9K4D4 | | (171) | DELHIVYTEFVSMMTQTAVDSRLLPL | 18 |
| Q9JXQ1 | | (167) | DRIHLVYSGFVNTMRQEPRMEVLLPI | 19 |
| Q9JW71 | | (167) | DRIHLVYSGFVNTMRQEPRMEVLLPI | 19 |
| Q9HT19 | | (166) | DRLFVVSNNKFVNTMTQKPTVEQLIPL | 14 |
| Q9FDR6 | | (186) | DQVHVYVTEFISMLTQNPVVHQLLPV | 16 |
| Q9FAA4 | | (186) | DQVHVYVTEFISMLTQNPVVHQLLPV | 16 |
| Q9CER9 | | (168) | DELYVCYNHHVNSLVSDARMEKMLPI | 18 |
| Q9ERA8 | | (181) | DEGSIIFNQFKSVISYKTEEKPIFSL | 21 |
| Q9D9D7 | | (181) | DEGSIIFNQFKSVISYKTEEKPIFSL | 21 |

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Block IPB000131E

| | | | |
|------------|---|--------|--|
| ID | ATPase_gamma; BLOCK | | |
| AC | IPB000131E; distance from previous block=(13,74) | | |
| DE | ATP synthase gamma subunit | | |
| BL | NQE; width=53; seqs=82; 99.5%=2428; strength=1518 | | |
| ATPG MYCGA | P33257 | (235) | LIESKVCEYASRRNAMDTAAKNADDLYNKYKLLYNQLRQAKITQEINEIVAGA 23 |
| ATPG PROMO | P29710 | (226) | ILENTASEHSARKNAMKNATDNAEDMIKDLTLQYNRERQAAITQEISEIVSGA 15 |
| ATPG RICPR | O50289 | (233) | LLQNIVSEEGARMTAMENATNNANDLISKLVKLNRSRQTIITTELIEIIAGA 31 |
| ATPG THIFE | P41169 | (233) | VIEHLACEQSARMVAMKSASDNAKRMVDDLQLAYNKARQAAITQEIAEISAGA 23 |
| ATPG CHLRE | P12113 | (301) | LQEALASELAARMNAMNNASDNAKELKKGLTVQYNKQRQAKITQELAEIVGGA 15 |
| ATPG ANASP | P12408 | (259) | LQESAASELAARMTAMSNASENAGELIKSLSYNKARQAAITQELLEVVGGA 13 |
| ATPG SPIPL | P50006 | (258) | WQESTASELAARMTAMSNASDNASDLVKTLTSLYNKARQASITQELLEVVAGA 14 |
| ATPG SYNPI | Q05384 | (259) | LQEAAAASELAARMTAMNNASDNAQTTLIGTLTSLYNKARQAAITQEILEVVAGA 14 |
| ATPG SYNPI | P08450 | (259) | LQEAAAASELAARMTAMNSASDNANALVGQTLVYNKARQAAITQELLEVVAGA 13 |
| ATPG SYNPI | P17253 | (259) | LQESAASELAARMTAMSNASDNAGQLIGTLTSLYNKARQAAITQELLEVVAGA 14 |
| ATPG BACCA | P41010 | (231) | LLDAKASEHAARMTAMKNATDNANDVIRTLTSLYNRARQAAITQEITEIVAGR 10 |
| ATPG BACFI | P22482 | (233) | LLDAKASEFGARMTAMSAATDNASALIEELTLKFNRRARQAAITQEITEIVGGA 12 |
| ATPG BACP3 | P09222 | (230) | LLDAKASEHAARMTAMKNATDNANELIRTLTSLYNRARQAAITQEITEIVAGA 8 |
| ATPG BUCAI | P57123 | (232) | I LENIASEHAARMIAMKTATDN SGNRIKELQLVYNKVRQANITQELNEIVSGA 13 |
| ATPG BUCAP | O51873 | (233) | L LENIASEQAARMVAMKTATDN SGNRIKELQLIYNKVRQANITQELTEIVAGA 12 |
| ATPG ECOLI | P00837 | (232) | VVENLASEQAARMVAMKAATDN GGS LIKELQLVYNKARQASITQELTEIVSGA 12 |
| ATPG VIBAL | P12990 | (233) | VVENLACEQAARMIAMKAATDNATNLIDDLVYNKARQAAITQELSEIVGGA 13 |
| ATPG MYCGE | P47640 | (226) | LVETKLCESASRQNAMEAATKNAKDLLDKYTLQFNKLRQNSITEEIIIEVIGGM 27 |
| ATPG MYCPN | Q50330 | (226) | LVETKLCESASRQNAMEAATKNAKDLLDKYTLQFNKLRQNSITQEIIIEIIGGI 26 |
| ATPG RHOBL | P05436 | (231) | LLENASEQGARMSAMDNATRNAGDMINKLTIQYNRSRQAAITKELIEIISGA 10 |
| ATPG RHOCB | P72246 | (235) | LLENNASFNQAQMSAMDNATRNAGDMIDRLTIEYNRSRQAAITKELIEIISGA 25 |
| ATPG RHORU | P07227 | (244) | MLESFASEQGARMTAMDNATRNAGDMIKKLSLTYNRTRQAQITKELIEIISGA 11 |
| ATP1 ARATH | Q01908 | (317) | LQESLASELAARMSAMSSASDNASDLKKSLSMVYNRKRQAKITGEILEIVAGA 15 |
| ATP2 ARATH | Q01909 | (328) | LQESLASELASRMNAMSNATDNVELKKNLTMAYNRARQAKITGELLEIVAGA 15 |
| ATPG PEA | P28552 | (318) | LQESLASELAARMSAMSSAFDNASELKTDLTRVYNRATQAKITGEILEIVAGD 37 |
| ATPG SPIOL | P05435 | (308) | LQESLASELAARMTAMSNATDNANELKKTLISINYNRARQAKITGEILEIVAGA 12 |
| ATPG TOBAC | P29790 | (321) | LQESLASELAARMSAMSSATDNATELKKNLRSVYNRQRQAKITGEILEIVAGA 12 |
| ATPG ODOSI | Q06908 | (314) | LQESVASELAARMQSMQSASDNAGDLAKRLSTEYNRARQAAVTQEILEIVSGA 23 |
| ATPG PHATR | Q41075 | (314) | LQESVASELAARMQSMQSASDNAGSLAKQLNLEYNRARQAAVTQELLEIISGA 23 |
| ATP3 ARATH | Q96250 | (266) | VLENACSEMGAARMSAMSSSRNAGEMLDRLTLTYNRTRQASITTELIEIISGA 18 |
| ATP3 IPOBA | P26360 | (269) | VLENACSEQGARMSAMSSSRNAGEMLDRLTLTYNRTRQASITTELIEIISGA 17 |
| ATPG BOVIN | P05631 | (242) | LKESTTSEQSARMTAMDNASKNASEMIDKLTTLTFNRTRQAVITKELIEIISGA 10 |
| ATPG HUMAN | P36542 | (242) | LKESTTSEQSARMTAMDNASKNASEMIDKLTTLTFNRTRQAVITKELIEIISGA 10 |
| ATPG RAT | P35435 | (217) | LKESTTSEQSARMTAMDNASKNASDMIDKLTTLTFNRTRQAVITKELIEIISGA 10 |
| ATPG KLULA | P49377 | (233) | MAEGYAAEVSARRNAMDNASKNAGDMINSYSILYNRTRQAVITNELVDIITGA 22 |
| ATPG YEAST | P38077 | (255) | MAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTRQAVITNELVDIITGA 23 |
| ATPG ACEWO | P50005 | (245) | MIESAASEQGARRTAMESATTNANEMIDGLTLQYNRVQAPITQEISEIVGGA 18 |
| ATPG BACME | P20602 | (229) | LLDGKASEHAARMTAMKSATDNAKDLINNLTLSYNRARQAAITQEITEIVGGA 9 |
| ATPG BACST | P42007 | (231) | LLDAKASEHAARMTAMKNATDNANDVIRTLTSLYNRARQAAITQEITEIVAGR 10 |
| ATPG BACSU | P37810 | (234) | LLDSKASEHAARMTAMKNATDNAKELIDSLSLSYNRARQAAITQEITEIVGGA 8 |
| ATPG ENTHR | P43452 | (244) | IVDAKTAEHAAGMTAMKTATDNAATI IDDLTVSYNRARQGAITQEITEIVAGA 20 |

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|-------------------|---------|---|-----|
| ATPG_HAEIN P43716 | (234) | VVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGA | 11 |
| ATPG_HELPY P56082 | (245) | LIDSLAAEHSARMQAMDTATNNAKDLVKTLTISYNKARQEAITTELVEINAGV | 16 |
| ATPG_HELPJ Q9ZK80 | (245) | LIDSLAAEHSARMQAMDTATNNAKDLVKTLTISYNKARQEAITTELVEINAGV | 16 |
| ATPG_MYCLE P45824 | (239) | MLESAASELASRQRAMKSATDNADDLIKALTLEANRERQAQITQEISEIVGGA | 14 |
| ATPG_MYCTU Q10597 | (246) | LLESAASELASRQRAMKSATDNADDLIKALTLMANRERQAQITQEISEIVGGA | 16 |
| ATPG_PASMU Q9L6B6 | (234) | AVENLASEQAARMVAMKAATDNAGNLINELQLVYNKARQASITNELNEIVAGA | 13 |
| ATPG_STRLI P50007 | (238) | LLQSAASKHAATRRAMKSATDNAGELINTLSRLANAARQAQITQEISEIVGGA | 22 |
| ATPG_STRMU P95788 | (236) | IIDAKTAEHAAGMTAMQTATDNADKVIEDLTKLYNRVRRQAQITQEITEIVAGA | 17 |
| ATPG_DROME O01666 | (241) | MKEGACSEQSSRMTAMDNASKNAGEMIDKLTFTFNRTRQAVITRELIEIISGA | 14 |
| O74754 | (245) | MAEAHCSEMSSRRNAMENASKSAGDMINKFSIQYNRQRQASITNELIDIVTGA | 38 |
| Q9NE84 | (228) | VCENELSEQAARLVAVEGQLSNISTLQQKTSSLYNKTRQSSITSSSLIEIISAM | 100 |
| O21267 | (221) | LIENVTSEQGARMNAMDNAAKNAGEMIDKLTLYNKAQASITSELIEIISCA | 18 |
| Q9G8R3 | (232) | LEENEYSALGARATAMNNATKNVSELIDRLRLSYNKAQETITNELIEIVSCV | 42 |
| O50141 | (229) | IVDSFASEQAARRTAMESASDNANEMIEKLSLLYNRARQAQITQEITEISSA | 19 |
| O50158 | (235) | IVDAKTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAQITQEITEIVAGA | 11 |
| O67829 | (233) | MVESNAAEHFARMIAMDNATKNAEDLIRQWTLVFNKARQEAITTELIDITNAV | 41 |
| O05432 | (226) | LLEAKASEHGARTAMDNATKNAEMIDKFTLSFNRRQAQITNEIVEIVAGA | 13 |
| Q52412 | (226) | LLDAKASEHAARTAMKNATDNANELIRTLTSLYNRARQAQITQEITEIVAGA | 8 |
| Q9ZJ02 | (237) | IIDAKTAENAAGMTAMQTATDNAKKVISDLTIQYNRARQAQITQEITEIVAGA | 13 |
| Q9Z688 | (226) | LLNSKASEQASRMSSMDSATKNANDLLDALNIKYNRIRQSAITQEITEIVGGA | 27 |
| Q9X1U6 | (213) | MFQTKIGEYYARQNAKMATDNQAQEVIRELTLAYNKAQASITQELIEIVTGA | 33 |
| Q9RQ80 | (232) | ILENIASEHAARMAMKTATENSTERIKELKLYNKVRQATITQELTEIISGA | 19 |
| Q9RQ77 | (232) | ILENCTCEQASRMISMKQATDNSEDLIKLRILYNKARQDNITQELTEIISGA | 23 |
| Q9RQ74 | (231) | SLENYTSEQAARMIAMKQATDNASKDLIRELQIILYNKARQDNITQELTEIVSGA | 19 |
| Q9RGY2 | (264) | ILDAKTAEHASSMTAMQSATDNANDLVSNTTKLNRARQAQITTEITEIISGA | 23 |
| Q9RFL4 | (232) | VVENLASEQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGA | 12 |
| Q9RAU1 | (234) | IVDAKTAEHAAGMTAMRTATDNAHSVINDLTIQYNRARQASITQEITEIVAGA | 14 |
| Q9PR14 | (232) | LIESKISENASRRNAMDAATKNAKALAENYKLIYNTLRQGKITREITEIVAGS | 29 |
| Q9PJ20 | (238) | LIDSLAAEHSARMQAMDNATNNAKARVKQLNLAYNKAQESITTELIEIISGV | 16 |
| Q9PE84 | (232) | MLENIASEHAARMVAMKAASDNANKLIGTLQLVYNKARQAQITQEISEIVGGA | 11 |
| Q9KNH4 | (233) | VVENLACEQAARMVAMKAATDNASNLIIDDLQLVYNKARQAQITQELSEIVGGA | 10 |
| Q9K6H4 | (229) | LLDAKASEFAARTAMSAATDNATNLIDELTSLYNRARQAQITQEITEIVGGA | 10 |
| Q9K4D4 | (241) | LLQSAASKHAATRRAMKSATDNAGELINTLSRLANAARQAQITQEISEIVGGA | 22 |
| Q9JXQ1 | (236) | LSDNMASEQAARMVAMKAATDNAGNAIKELRLVYNKSRQAQITTELSEIVAGA | 14 |
| Q9JW71 | (236) | LSDNMASEQAARMVAMKAATDNAGNAIKELRLVYNKSRQAQITTELSEIVAGA | 14 |
| Q9HT19 | (231) | VVENNACEQAARMIAMKNATDNAGELISDLQLIYNKARQAQITQEISEIVGGA | 11 |
| Q9FDR6 | (263) | FLEAAAAESASRRNAMKSATDNATELVKDLSRVANQARQAQITQEITEIVGGA | 16 |
| Q9FAA4 | (263) | FLEAAAAESASRRNAMKSATDNATELVKDLSRVANQARQAQITQEITEIVGGA | 16 |
| Q9CER9 | (234) | IVDAKTAEHAAGMTAMRTATDNAHSVINDLTIQYNRARQASITQEITEIVAGA | 14 |
| Q9ERA8 | (242) | LKESTTSEQSARMTAMDNASKNASDMIDKLTFTFNRTRQAVITKELIEIISGA | 10 |
| Q9D9D7 | (242) | LKESTTSEQSARMTAMDNASKNASDMIDKLTFTFNRTRQAVITKELIEIISGA | 10 |

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COBBLER sequence (region containing Blocks only)

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COBBLER sequence:

```
>IPB000131 ATPG_BACME|P20602 from 1 to 285 with embedded consensus blocks
masLKEIKRRIKSVKNTQKITKAMKMVAAAKLRKAeqnaksfvpymekiqevvssvalgsrgashpmltarsVKKTLYIV
ITSDRGLCGGYNSNVIKkvsqaeerhqspsdeygviaIGKKGMSYFKRRgipvlleitgladqpafadiqqiasqtvqmf
```


adgtfDEVYIIYNKFVNAISQEPTVKQLLPLtdlqpsgklvgfefpsqeeilevllpqaesliyyggLESKASEHAAR
MTAMENATDNAGDLIKKLTlVYNRARQAAITQELIEIVSGAaale

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[MetaFam IPB000131](#)

IPB000131B : [CYRCA IPB000131B](#)

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|-----|-------|--|
| S1 | 21 | (COUPLING? (3N) FACTOR?) AND (ACTINOBACILL? OR HAEMOPHIL? - OR MANNHEIM? OR PASTEURELL? OR MULTOCIDA? OR INFLUENZAE?) |
| S2 | 7 | S1/2000:2003 |
| S3 | 14 | S1 NOT S2 |

?t s3/9/1

3/9/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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10961712 BIOSIS NO.: 199799582857

Identification and characterization of the putative transcription-repair-coupling factor gene (trcL) of *Listeria monocytogenes*.

AUTHOR: Zheng W; Kathariou S

AUTHOR ADDRESS: Univ. Hawaii, Honolulu, HI**USA

JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 97 (0):p362 1997

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ISSN: 1060-2011

RECORD TYPE: Citation

LANGUAGE: English

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Physiology

BIOSYSTEMATIC NAMES: Endospore-forming Gram-Positives--Eubacteria, Bacteria; Enterobacteriaceae--Eubacteria, Bacteria; **Pasteurellaceae** -- Eubacteria, Bacteria; Regular Nonsporing Gram-Positive Rods--Eubacteria, Bacteria

ORGANISMS: endospore-forming gram-positive rods and cocci (Endospore-forming Gram-Positives); regular nonsporing gram-positive rods (Regular Nonsporing Gram-Positive Rods); *Bacillus subtilis* (Endospore-forming Gram-Positives); *Escherichia coli* (Enterobacteriaceae); ***Haemophilus influenzae*** (***Pasteurellaceae***); *Listeria monocytogenes* (Regular Nonsporing Gram-Positive Rods

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms

MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence; nucleotide sequence


MISCELLANEOUS TERMS: Meeting Abstract; Meeting Poster; CHARACTERIZATION ; CHEMICAL COORDINATION; COLD STRESS; COLD STRESS RESPONSE GENE; FOOD CONTAMINANT; IDENTIFICATION; IN FRAME DELETION MUTANT; LTRA GENE; LTRB GENE; LTRC GENE; MOLECULAR GENETICS; TRANSCRIPTION-REPAIR- **COUPLING FACTOR** ; TRANSCRIPTION-REPAIR- **COUPLING FACTOR** GENE; TRCL GENE; TRCL GENE PRODUCT

CONCEPT CODES:

10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10616 External Effects-Temperature as a Primary Variable-Cold (1971-)
23010 Temperature: Its Measurement, Effects and Regulation-Thermoadaptation
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
00520 General Biology-Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals

BIOSYSTEMATIC CODES:

06702 Enterobacteriaceae (1992-)
06703 **Pasteurellaceae** (1992-)
07810 Endospore-forming Gram-Positives (1992-)
07830 Regular Nonsporing Gram-Positive Rods (1992

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ATP synthase gamma subunit signature

| PROSITE cross-reference(s) | |
|---|---|
| <u>PS00153; ATPASE GAMMA</u> | |
| Documentation | |
| <p>ATP synthase (proton-translocating ATPase) (EC 3.6.3.14) [1,2] is a component of the cytoplasmic membrane of eubacteria, the inner membrane of mitochondria, and the thylakoid membrane of chloroplasts. The ATPase complex is composed of an oligomeric transmembrane sector, called CF(0), and a catalytic core, called coupling factor CF(1). The former acts as a proton channel; the latter is composed of five subunits, alpha, beta, gamma, delta and epsilon. Subunit gamma is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex. The best conserved region of the gamma subunit [3] is its C-terminus which seems to be essential for assembly and catalysis. As a signature pattern to detect ATPase gamma subunits, we used a 14 residue conserved segment where the last amino acid is found one to three residues from the C-terminal extremity.</p> | |
| Description of pattern(s) and/or profile(s) | |
| Consensus pattern | [IV]-T-x-E-x(2)-[DE]-x(3)-G-A-x-[SAKR] |
| Sequences known to belong to this class detected by the pattern | ALL, except for pea chloroplast gamma and two Bacillus species gamma. |